STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/606,910 F_

Source: _1FW16_

Date Processed by STIC: _4/5/07_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE __CHECKER VERSION 4.4.0 PROGRAM__, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual - ePAVE).
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/606,910F_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_✓__Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering   use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
ensure your subsequent submission is saved in ASCII text.

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
each n or Xaa can only represent a single residue. Please present the maximum number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.

7____Skipped Sequences   Sequence(s)_____missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown).
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences   Sequence(s)_____missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
is Artificial Sequence. (see item 11 below)

11____Use of <220>   Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use
of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
Sequence Rules

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – STIC Systems Branch – 03/02/06

IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/606,910P

DATE: 04/05/2007
TIME: 10:02:12

Input Set : A:\050185Sequence.txt
Output Set: N:\CRF4\04052007\I606910P.raw

```
     3 <110> APPLICANT: Max-Delbrueck-Centrum fuer Molekulare Medizin
     5 <120> TITLE OF INVENTION: Tumor vaccines for mucl-positive carcinomas
     7 <130> FILE REFERENCE: 0107-027
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/606,910P
    10 <141> CURRENT FILING DATE: 2000-06-29
    12 <150> PRIOR APPLICATION NUMBER: DE 197 58 400.4
    13 <151> PRIOR FILING DATE: 1997-12-30
    15 <150> PRIOR APPLICATION NUMBER: PCT/DE98/03819
    16 <151> PRIOR FILING DATE: 1998-12-30
    18 <160> NUMBER OF SEQ ID NOS: 6
    20 <170> SOFTWARE: PatentIn Ver. 2.1
```

see pp 1-2

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
    22 <210> SEQ ID NO: 1
    23 <211> LENGTH: 7
    24 <212> TYPE: PRT
    25 <213> ORGANISM: human
    27 <220> FEATURE:
    28 <223> OTHER INFORMATION: immunodominant region of MUC1
    30 <400> SEQUENCE: 1
    31 Pro Asp Thr Arg Pro Ala Pro
B--> 32 1           5       5
    34 <210> SEQ ID NO: 2
    35 <211> LENGTH: 8
    36 <212> TYPE: PRT
    37 <213> ORGANISM: mouse, IgG1
    39 <220> FEATURE:
    40 <223> OTHER INFORMATION: A76-A/C7 epitope
    42 <400> SEQUENCE: 2
    43 Ala Pro Asp Thr Arg Pro Ala Pro
B--> 44 1     5       5
    47 <210> SEQ ID NO: 3
    48 <211> LENGTH: 6
    49 <212> TYPE: PRT
    50 <213> ORGANISM: mouse, IgG1
    52 <220> FEATURE:
    53 <223> OTHER INFORMATION: MF06 epitope
    55 <400> SEQUENCE: 3
    56 Asp Thr Arg Pro Ala Pro
B--> 57 1   5       5
    59 <210> SEQ ID NO: 4
```

misaligned amino acid numbers (see item 3 on Error Summary Sheet)

misaligned numbers

misaligned

RAW SEQUENCE LISTING   DATE: 04/05/2007
PATENT APPLICATION: US/09/606,910P   TIME: 10:02:12

Input Set : A:\050185Sequence.txt
Output Set: N:\CRF4\04052007\I606910P.raw

```
   60 <211> LENGTH: 21
   61 <212> TYPE: PRT
   62 <213> ORGANISM: Artificial Sequence
   64 <220> FEATURE:
   65 <223> OTHER INFORMATION: Description of Artificial Sequence: designed
   66       synthetical glycopeptide
   68 <400> SEQUENCE: 4
   69 Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser
E--> 70 1  5  10  15      5                   10                  15
   72 Thr Ala Pro Pro Ala        misaligned numbers
E--> 73    20        20
   75 <210> SEQ ID NO: 5
   76 <211> LENGTH: 20
   77 <212> TYPE: PRT
   78 <213> ORGANISM: Artificial Sequence
   80 <220> FEATURE:
   81 <223> OTHER INFORMATION: Description of Artificial Sequence: designed
   82       synthetical glycopeptide
   84 <400> SEQUENCE: 5
   85 His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr
E--> 86 1  5  10  15     5                    10                  15
   88 Ala Pro Pro Ala        misaligned    10
E--> 89    20        20
   93 <210> SEQ ID NO: 6
   94 <211> LENGTH: 7
   95 <212> TYPE: PRT
   96 <213> ORGANISM: human
   98 <220> FEATURE:
   99 <221> NAME/KEY: DOMAIN
  100 <222> LOCATION: (1) .. (7)
  101 <223> OTHER INFORMATION: immunodominant motif of the epithelial mucin (
  102       MUC1)
  104 <400> SEQUENCE: 6
  105 Pro Asp Thr Arg Pro Ala Pro
E--> 106 1  5                    5
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/606,910F

DATE: 04/05/2007
TIME: 10:02:13

Input Set : A:\050185Sequence.txt
Output Set: N:\CRF4\04052007\I606910F.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:32 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:44 M:932 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:57 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:70 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
L:73 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
L:86 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:89 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:106 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6

* *

Reviewer Comments:

<210> 2

<211> 8

<212> PRT

<213> mouse, IgG1

<220>

<223> A76-A/C7 epitope

<400> 2

Ala Pro Asp Thr Arg Pro Ala Pro

 1   5

<210> 3

<211> 6

<212> PRT

<213> mouse, IgG1

<220>

<223> MF06 epitope

<400> 3

Asp Thr Arg Pro Ala Pro

 1   5

Remove the ", IgG1" from the response for numeric identifier <213> in
SEQ ID # 2 and 3.

For SEQ ID # 1, 2, and 3 add numeric identiers <221> and <222> to the
feature.

* *